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SEQUENCE LISTING



<110> SUNTORY LIMITED

TECH CENTER 1600/2900

<120> Gene coding for a protein having glycosyl transferase to aurone

<160> 6

<210> 1

<211> 1751

<212> DNA

<213> Antirrhinum majus

br
<220>

<223> Nucleotide sequence coding for a protein having glycosyl transferase to aurone

<400> 1

ctcacttagt actaaaacac aaaactgaga acccttcaaa tttccacttg atcatattca 60
attttccttt taaaa atg gga aaa ctt cac att gcc tta ttt cca gtt atg 111
Met Gly Lys Leu His Ile Ala Leu Phe Pro Val Met

1 5 10

gct cat ggt cac atg atc cca atg ttg gac atg gcc aag ctc ttt acc 159
Ala His Gly His Met Ile Pro Met Leu Asp Met Ala Lys Leu Phe Thr
15 20 25

tca aga ggc ata caa aca aca atc att tcg act ctc gcc ttc gct gat 207
Ser Arg Gly Ile Gln Thr Thr Ile Ile Ser Thr Leu Ala Phe Ala Asp
30 35 40

ccg ata aac aaa gct cgt gat tcg ggc ctc gat att gga cta agc atc 255
Pro Ile Asn Lys Ala Arg Asp Ser Gly Leu Asp Ile Gly Leu Ser Ile
45 50 55 60

ctc aaa ttc cca cca gaa gga tca gga ata cca gat cac atg gtg agc 303
Leu Lys Phe Pro Pro Glu Gly Ser Gly Ile Pro Asp His Met Val Ser
65 70 75

ctt gat cta gtt act gaa gat tgg ctc cca aag ttt gtt gag tca tta	80	85	90	351
Leu Asp Leu Val Thr Glu Asp Trp Leu Pro Lys Phe Val Glu Ser Leu				
gta ttc tta caa gag cca gtt gag aag ctt atc gaa gaa cta aag ctc	95	100	105	399
Val Leu Leu Gln Glu Pro Val Glu Lys Leu Ile Glu Glu Leu Lys Leu				
gac tgt ctc gtt tcc gac atg ttc ttg cct tgg aca gtc gat tgt gcg	110	115	120	447
Asp Cys Leu Val Ser Asp Met Phe Leu Pro Trp Thr Val Asp Cys Ala				
gct aag ttc ggt att ccg agg ttg gtt ttc cac gga acg acg aac ttt	125	130	135	495
Ala Lys Phe Gly Ile Pro Arg Leu Val Phe His Gly Thr Ser Asn Phe				
gcg ttg tgt gct tcg gag caa atg aag ctt cac aag cct tat aag aat	145	150	155	543
Ala Leu Cys Ala Ser Glu Gln Met Lys Leu His Lys Pro Tyr Lys Asn				
gta act tct gat act gag aca ttt gtt ata ccg gat ttc ccg cat gag	160	165	170	591
val Thr Ser Asp Thr Glu Thr Phe Val Ile Pro Asp Phe Pro His Glu				
ctg aag ttt gtg agg act caa gtg gct ccg ttt cag ctt gcg gaa acg	175	180	185	639
Leu Lys Phe Val Arg Thr Gln Val Ala Pro Phe Gln Leu Ala Glu Thr				
gag aat gga ttc tca aag ttg atg aaa cag atg acg gag tct gtt ggt	190	195	200	687
Glu Asn Gly Phe Ser Lys Leu Met Lys Gln Met Thr Glu Ser Val Gly				
aga agc tac ggt gtt gtg gtt aac agt ttt tat gag ctc gag tcg act	205	210	215	735
Arg Ser Tyr Gly Val Val Asn Ser Phe Tyr Glu Leu Glu Ser Thr				
tat gtg gat tat tac aga gag gtt ttg ggt aga aag tct tgg aat ata	225	230	235	783
Tyr Val Asp Tyr Tyr Arg Glu Val Leu Gly Arg Lys Ser Trp Asn Ile				
ggg cct ctg ttg tta tcc aac aat ggc aat gag gaa aaa gta caa agg	240	245	250	831
Gly Pro Leu Leu Ser Asn Asn Gly Asn Glu Glu Lys Val Gln Arg				
gga aag gaa tct gcg att ggc gaa cac gaa tgc ttg gct tgg ttg aat	255	260	265	879
Gly Lys Glu Ser Ala Ile Gly Glu His Glu Cys Leu Ala Trp Leu Asn				

tcc aag aag cag aat tcg gtt gtt tac gtt ttt gga agt atg gcg	927
Ser Lys Lys Gln Asn Ser Val Val Tyr Val Cys Phe Gly Ser Met Ala	
270 275 280	
act ttt act cca gcg cag ttg cgc gaa act gcg att gga ctc gag gaa	975
Thr Phe Thr Pro Ala Gln Leu Arg Glu Thr Ala Ile Gly Leu Glu Glu	
285 290 295 300	
tca ggc caa gag ttc att tgg gta gtt aaa aag gcc aaa aac gaa gaa	1023
Ser Gly Gln Glu Phe Ile Trp Val Val Lys Lys Ala Lys Asn Glu Glu	
305 310 315	
gaa gga aaa gga aaa gaa gaa tgg ctg cca gaa aat ttt gag gaa aga	1071
Glu Gly Lys Gly Lys Glu Trp Leu Pro Glu Asn Phe Glu Glu Arg	
320 325 330	
gtg aaa gat aga ggc ttg atc ata aga gga tgg gcg ccg caa ttg ttg	1119
Val Lys Asp Arg Gly Leu Ile Ile Arg Gly Trp Ala Pro Gln Leu Leu	
335 340 345	
ata ctc gat cat cct gcg gta gga gct ttc gtg acg cat tgt gga tgg	1167
Ile Leu Asp His Pro Ala Val Gly Ala Phe Val Thr His Cys Gly Trp	
350 355 360	
aat tcg acg ttg gaa gga ata tgc gcc ggt gtg cct atg gtg act tgg	1215
Asn Ser Thr Leu Glu Gly Ile Cys Ala Gly Val Pro Met Val Thr Trp	
365 370 375 380	
cca gtt ttc gca gag cag ttt ttc aat gag aag ttt gtg aca gag gtt	1263
Pro Val Phe Ala Glu Gln Phe Phe Asn Glu Lys Phe Val Thr Glu Val	
385 390 395	
ttg ggg acc ggt gtt tcg gtt ggg aat aag aag tgg cta agg gca gca	1311
Leu Gly Thr Gly Val Ser Val Gly Asn Lys Lys Trp Leu Arg Ala Ala	
400 405 410	
agt gaa ggt gtg tcg agg gag gca gtg acg aac gcg gtg cag cgt gtt	1359
Ser Glu Gly Val Ser Arg Glu Ala Val Thr Asn Ala Val Gln Arg Val	
415 420 425	
atg gtg gga gaa aat gcg tcg gag atg aga aag cga gcg aag tat tat	1407
Met Val Gly Glu Asn Ala Ser Glu Met Arg Lys Arg Ala Lys Tyr Tyr	
430 435 440	
aag gaa atg gcg agg cgg gcg gtt gag gaa ggc ggt tcg tct tat aat	1455
Lys Glu Met Ala Arg Arg Ala Val Glu Glu Gly Gly Ser Ser Tyr Asn	
445 450 455 460	

ggt ttg aat gag atg ata gag gat ttg agt gtg tac cgt gct cca gaa 1503
Gly Leu Asn Glu Met Ile Glu Asp Leu Ser Val Tyr Arg Ala Pro Glu
465 470 475
aaa caa gac tta aac tagattctta tagatgactt ctagtgtgac aattgtaatt 1558
Lys Gln Asp Leu Asn
480
ttttgcctt tattcaagtt tcctcattag tgttgagagc tttccctgta tttcagaat 1618
tggtttgttc aattttaca tgatttgtga tagatacgctg catagttct agctgttaac 1678
attgtttgat catattgagt tgatttaaaa tgagagtagc atgtgatctt cagattaaaa 1738
aaaaaaaaaaa aaa 1751

<210> 2

<211> 481

<212> PRT

<213> Antirrhinum majus

<220>

<223> Amino acid sequence of a protein having glycosyl
transferase to aurone

<400> 2

Met Gly Lys Leu His Ile Ala Leu Phe Pro Val Met Ala His Gly His

1 5 10 15

Met Ile Pro Met Leu Asp Met Ala Lys Leu Phe Thr Ser Arg Gly Ile

20 25 30

Gln Thr Thr Ile Ile Ser Thr Leu Ala Phe Ala Asp Pro Ile Asn Lys

35 40 45

Ala Arg Asp Ser Gly Leu Asp Ile Gly Leu Ser Ile Leu Lys Phe Pro

50 55 60

Pro Glu Gly Ser Gly Ile Pro Asp His Met Val Ser Leu Asp Leu Val

65 70 75 80

Thr Glu Asp Trp Leu Pro Lys Phe Val Glu Ser Leu Val Leu Leu Gln

85 90 95

Glu Pro Val Glu Lys Leu Ile Glu Glu Leu Lys Leu Asp Cys Leu Val

100 105 110

Ser Asp Met Phe Leu Pro Trp Thr Val Asp Cys Ala Ala Lys Phe Gly
115 120 125
Ile Pro Arg Leu Val Phe His Gly Thr Ser Asn Phe Ala Leu Cys Ala
130 135 140
Ser Glu Gln Met Lys Leu His Lys Pro Tyr Lys Asn Val Thr Ser Asp
145 150 155 160
Thr Glu Thr Phe Val Ile Pro Asp Phe Pro His Glu Leu Lys Phe Val
165 170 175
Arg Thr Gln Val Ala Pro Phe Gln Leu Ala Glu Thr Glu Asn Gly Phe
180 185 190
Ser Lys Leu Met Lys Gln Met Thr Glu Ser Val Gly Arg Ser Tyr Gly
195 200 205
Val Val Val Asn Ser Phe Tyr Glu Leu Glu Ser Thr Tyr Val Asp Tyr
210 215 220
Tyr Arg Glu Val Leu Gly Arg Lys Ser Trp Asn Ile Gly Pro Leu Leu
225 230 235 240
Leu Ser Asn Asn Gly Asn Glu Glu Lys Val Gln Arg Gly Lys Glu Ser
245 250 255
Ala Ile Gly Glu His Glu Cys Leu Ala Trp Leu Asn Ser Lys Lys Gln
260 265 270
Asn Ser Val Val Tyr Val Cys Phe Gly Ser Met Ala Thr Phe Thr Pro
275 280 285
Ala Gln Leu Arg Glu Thr Ala Ile Gly Leu Glu Ser Gly Gln Glu
290 295 300
Phe Ile Trp Val Val Lys Lys Ala Lys Asn Glu Glu Glu Gly Lys Gly
305 310 315 320
Lys Glu Glu Trp Leu Pro Glu Asn Phe Glu Glu Arg Val Lys Asp Arg
325 330 335
Gly Leu Ile Ile Arg Gly Trp Ala Pro Gln Leu Leu Ile Leu Asp His
340 345 350
Pro Ala Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu
355 360 365
Glu Gly Ile Cys Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala
370 375 380
Glu Gln Phe Phe Asn Glu Lys Phe Val Thr Glu Val Leu Gly Thr Gly
385 390 395 400
Val Ser Val Gly Asn Lys Lys Trp Leu Arg Ala Ala Ser Glu Gly Val
405 410 415

Ser Arg Glu Ala Val Thr Asn Ala Val Gln Arg Val Met Val Gly Glu
420 425 430
Asn Ala Ser Glu Met Arg Lys Arg Ala Lys Tyr Tyr Lys Glu Met Ala
435 440 445
Arg Arg Ala Val Glu Glu Gly Ser Ser Tyr Asn Gly Leu Asn Glu
450 455 460
Met Ile Glu Asp Leu Ser Val Tyr Arg Ala Pro Glu Lys Gln Asp Leu
465 470 475 480
Asn

<210> 3
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400>
ataactacat atgggacaac tccac

25

<210> 4
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 4
cagaacagga tccacacgta attta

25

<210> 5
<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer
<400> 5
ataaactacat atgggaaaac ttcac

25

<210> 6
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 6
gaacaggatc cacacactag aagtca

26

<210> 7
<211> 1750
<212> DNA
<213> Petunia hybrida

<220>
<223> Nucleotide sequence coding for a protein having
glycosyl transferase to aurone

<400> 7
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Met Ala Ile Pro Thr Val
1 5

caa cca cat ttt gtg ctg ctt cct ttc atg gca caa ggc cat aca aat	10	15	20	101
Gln Pro His Phe Val Leu Leu Pro Phe Met Ala Gln Gly His Thr Asn				
ccc atg att gac atc gca cgc cta ttg gca caa cgc gga gtt ata atc	25	30	35	149
Pro Met Ile Asp Ile Ala Arg Leu Leu Ala Gln Arg Gly Val Ile Ile				
acc att ctt act aca cac ttt aat gcc act aga ttc aag aca gtc gtt	40	45	50	197
Thr Ile Leu Thr Thr His Phe Asn Ala Thr Arg Phe Lys Thr Val Val				
gat cgg gca gta gtg gca cta aag att cag gta gtt cac ctc tat	55	60	65	245
Asp Arg Ala Val Val Ala Ala Leu Lys Ile Gln Val Val His Leu Tyr				
ttt cca agc tta gag gct gga cta cct gaa ggg tgt gaa gct ttc gac	75	80	85	293
Phe Pro Ser Leu Glu Ala Gly Leu Pro Glu Gly Cys Glu Ala Phe Asp				
atg ctt cct tca atg gat ttc gca atg aaa ttc ttt gat gct acc agt	90	95	100	341
Met Leu Pro Ser Met Asp Phe Ala Met Lys Phe Phe Asp Ala Thr Ser				
agg ctt caa cca caa gtg gaa gaa atg ctt cat gaa ctg caa ccg tca	105	110	115	389
Arg Leu Gln Pro Gln Val Glu Glu Met Leu His Glu Leu Gln Pro Ser				
cca agt tgc ata ata tct gat atg tgt ttt cca tgg aca act aat gtt	120	125	130	437
Pro Ser Cys Ile Ile Ser Asp Met Cys Phe Pro Trp Thr Thr Asn Val				
gca caa aaa ttc aac att cct agg ctt gtt ttt cat ggg atg tgc tgt	135	140	145	485
Ala Gln Lys Phe Asn Ile Pro Arg Leu Val Phe His Gly Met Cys Cys				
ttt tct tta ttg tgc ttg cac aat ttg aga gat tgg aag gag ttg gag	155	160	165	533
Phe Ser Leu Leu Cys Leu His Asn Leu Arg Asp Trp Lys Glu Leu Glu				
tct gat ata gaa tat ttt caa gtt cca gga tta cat gac aaa att gaa	170	175	180	581
Ser Asp Ile Glu Tyr Phe Gln Val Pro Gly Leu His Asp Lys Ile Glu				
tta aac aaa gct cag ctt tca aat att gtt aag cca aga ggt cct gat	185	190	195	629
Leu Asn Lys Ala Gln Leu Ser Asn Ile Val Lys Pro Arg Gly Pro Asp				

tgg aat gaa ttt gca gat caa ctg aag aaa gca gaa gaa gaa gct tat			677
Trp Asn Glu Phe Ala Asp Gln Leu Lys Lys Ala Glu Glu Glu Ala Tyr			
200	205	210	
ggg ata gta gct aat agc ttt gaa gag tta gaa cca gaa tat gtc aag			725
Gly Ile Val Ala Asn Ser Phe Glu Glu Leu Glu Pro Glu Tyr Val Lys			
215	220	225	230
gga ttg gaa aag gca aaa ggc ttg aaa att tgg cca att ggt cct gtt			773
Gly Leu Glu Lys Ala Lys Gly Leu Lys Ile Trp Pro Ile Gly Pro Val			
235	240	245	
tct ttg tgc aac aaa gag aaa cag gac aag gct gaa aga gga aac aag			821
Ser Leu Cys Asn Lys Glu Lys Gln Asp Lys Ala Glu Arg Gly Asn Lys			
250	255	260	
gct tca att gat gaa cac cag tgt cta aaa tgg cta gat tct tgg gga			869
Ala Ser Ile Asp Glu His Gln Cys Leu Lys Trp Leu Asp Ser Trp Gly			
265	270	275	
gca aac tct gta ctc ttt gta tgt ctc ggg agc cta tcg cgc ctt cca			917
Ala Asn Ser Val Leu Phe Val Cys Leu Gly Ser Leu Ser Arg Leu Pro			
280	285	290	
acg cca caa atg ata gag ctg gga ctt ggc tta gaa tcg tcg aaa aga			965
Thr Pro Gln Met Ile Glu Leu Gly Leu Gly Leu Glu Ser Ser Lys Arg			
295	300	305	310
ccc ttt att tgg gtt aga cac aag tca gat gaa ttt aaa agt tgg			1013
Pro Phe Ile Trp Val Val Arg His Lys Ser Asp Glu Phe Lys Ser Trp			
315	320	325	
cta gtt gaa gaa aat ttt gag gaa aga gtt aaa gga caa gga ctt tta			1061
Leu Val Glu Glu Asn Phe Glu Glu Arg Val Lys Gly Gln Gly Leu Leu			
330	335	340	
atc cat ggt tgg gca cca caa gta cta ata tta tct cac act tca att			1109
Ile His Gly Trp Ala Pro Gln Val Leu Ile Leu Ser His Thr Ser Ile			
345	350	355	
gga gga ttc ttg act cat tgt gga tgg aat tcg agt gtc gaa gga ata			1157
Gly Gly Phe Leu Thr His Cys Gly Trp Asn Ser Ser Val Glu Gly Ile			
360	365	370	
tct gca ggc gtt cca atg atc act tgg cca atg ttt gct gaa caa ttc			1205
Ser Ala Gly Val Pro Met Ile Thr Trp Pro Met Phe Ala Glu Gln Phe			
375	380	385	390

tgt aat gaa agg cta ata gtg aat gta ctg aag aca gga gta aag gct	1253		
Cys Asn Glu Arg Leu Ile Val Asn Val Leu Lys Thr Gly Val Lys Ala			
395	400	405	
gga att gag aat cct gtt atg ttt gga gag gaa gaa aaa gtt gga gca	1301		
Gly Ile Glu Asn Pro Val Met Phe Gly Glu Glu Lys Val Gly Ala			
410	415	420	
caa gtg agc aaa gat gat att aag atg gtt att gaa aga gtc atg ggc	1349		
Gln Val Ser Lys Asp Asp Ile Lys Met Val Ile Glu Arg Val Met Gly			
425	430	435	
gaa gaa gag gaa gct gaa atg aga aga aaa aga gca aaa gag tta gga	1397		
Glu Glu Glu Ala Glu Met Arg Arg Lys Arg Ala Lys Glu Leu Gly			
440	445	450	
gaa aag gca aag agg gct atg gag gaa ggg ggt tcc tca cac ttc aac	1445		
Glu Lys Ala Lys Arg Ala Met Glu Glu Gly Gly Ser Ser His Phe Asn			
455	460	465	470
ttg aca cag ttg att caa gat gtc act gag caa gca aat att tta aaa	1493		
Leu Thr Gln Leu Ile Gln Asp Val Thr Glu Gln Ala Asn Ile Leu Lys			
475	480	485	
tcc atc taggattata aagtcgattc caagttcctt ttacgatcaa tttctaacca	1549		
Ser Ile			
tctactagag atggtaacaa tccaaactgc gcctttttg cacaataatt attgtttat	1609		
gttcagctag cacaaaaagt ttactattag tagaaatatt tcagctggaa ctgccgaact	1669		
gctatgtaca ctgatggaac aatgtatgtc atgctattca attaactct gagctgaaaa	1729		
tatcatatacg gagctgattt t	1750		

<210> 8

<211> 488

<212> PRT

<213> Petunia hybrida

<220>

<223> Amino acid sequence of a protein having glycosyl transferase to aurone

<400> 8

Met Ala Ile Pro Thr Val Gln Pro His Phe Val Leu Leu Pro Phe Met
 1 5 10 15
 Ala Gln Gly His Thr Asn Pro Met Ile Asp Ile Ala Arg Leu Leu Ala
 20 25 30
 Gln Arg Gly Val Ile Ile Thr Ile Leu Thr Thr His Phe Asn Ala Thr
 35 40 45
 Arg Phe Lys Thr Val Val Asp Arg Ala Val Val Ala Ala Leu Lys Ile
 50 55 60
 Gln Val Val His Leu Tyr Phe Pro Ser Leu Glu Ala Gly Leu Pro Glu
 65 70 75 80
 Gly Cys Glu Ala Phe Asp Met Leu Pro Ser Met Asp Phe Ala Met Lys
 85 90 95
 Phe Phe Asp Ala Thr Ser Arg Leu Gln Pro Gln Val Glu Glu Met Leu
 100 105 110
 His Glu Leu Gln Pro Ser Pro Ser Cys Ile Ile Ser Asp Met Cys Phe
 115 120 125
 Pro Trp Thr Thr Asn Val Ala Gln Lys Phe Asn Ile Pro Arg Leu Val
 130 135 140
 Phe His Gly Met Cys Cys Phe Ser Leu Leu Cys Leu His Asn Leu Arg
 145 150 155 160
 Asp Trp Lys Glu Leu Glu Ser Asp Ile Glu Tyr Phe Gln Val Pro Gly
 165 170 175
 Leu His Asp Lys Ile Glu Leu Asn Lys Ala Gln Leu Ser Asn Ile Val
 180 185 190
 Lys Pro Arg Gly Pro Asp Trp Asn Glu Phe Ala Asp Gln Leu Lys Lys
 195 200 205
 Ala Glu Glu Ala Tyr Gly Ile Val Ala Asn Ser Phe Glu Glu Leu
 210 215 220
 Glu Pro Glu Tyr Val Lys Gly Leu Glu Lys Ala Lys Gly Leu Lys Ile
 225 230 235 240
 Trp Pro Ile Gly Pro Val Ser Leu Cys Asn Lys Glu Lys Gln Asp Lys
 245 250 255
 Ala Glu Arg Gly Asn Lys Ala Ser Ile Asp Glu His Gln Cys Leu Lys
 260 265 270
 Trp Leu Asp Ser Trp Gly Ala Asn Ser Val Leu Phe Val Cys Leu Gly
 275 280 285
 Ser Leu Ser Arg Leu Pro Thr Pro Gln Met Ile Glu Leu Gly Leu Gly
 290 295 300

Leu Glu Ser Ser Lys Arg Pro Phe Ile Trp Val Val Arg His Lys Ser
305 310 315 320
Asp Glu Phe Lys Ser Trp Leu Val Glu Glu Asn Phe Glu Glu Arg Val
325 330 335
Lys Gly Gln Gly Leu Leu Ile His Gly Trp Ala Pro Gln Val Leu Ile
340 345 350
Leu Ser His Thr Ser Ile Gly Gly Phe Leu Thr His Cys Gly Trp Asn
355 360 365
Ser Ser Val Glu Gly Ile Ser Ala Gly Val Pro Met Ile Thr Trp Pro
370 375 380
Met Phe Ala Glu Gln Phe Cys Asn Glu Arg Leu Ile Val Asn Val Leu
385 390 395 400
Lys Thr Gly Val Lys Ala Gly Ile Glu Asn Pro Val Met Phe Gly Glu
405 410 415
Glu Glu Lys Val Gly Ala Gln Val Ser Lys Asp Asp Ile Lys Met Val
420 425 430
Ile Glu Arg Val Met Gly Glu Glu Glu Ala Glu Met Arg Arg Lys
435 440 445
Arg Ala Lys Glu Leu Gly Glu Lys Ala Lys Arg Ala Met Glu Glu Gly
450 455 460
Gly Ser Ser His Phe Asn Leu Thr Gln Leu Ile Gln Asp Val Thr Glu
465 470 475 480
Gln Ala Asn Ile Leu Lys Ser Ile
485

<210> 9

<211> 1669

<212> DNA

<213> Petunia hybrida

<220>

<223> Nucleotide sequence coding for a protein having
glycosyl transferase to aurone

<400> 9

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tgcttaagtac tactactagt acacatctt ctttatca aacacttcc aaa atg	116
Met	
1	
ggt cag ctc cat ttt ttc ttc ttt ccc atg atg gct cat ggc cac atg	164
Gly Gln Leu His Phe Phe Phe Pro Met Met Ala His Gly His Met	
5 10 15	
att cct aca cta gac atg gct aag ctt ttc gct tca cgt ggt gtt aag	212
Ile Pro Thr Leu Asp Met Ala Lys Leu Phe Ala Ser Arg Gly Val Lys	
20 25 30	
gcc acc ata atc act act cct ctc aat gaa tca gtt ttc tcc aaa gct	260
Ala Thr Ile Ile Thr Thr Pro Leu Asn Glu Ser Val Phe Ser Lys Ala	
35 40 45	
att gaa aga aac aag cat gaa att gac atc cgt ttg atc aaa ttc caa	308
Ile Glu Arg Asn Lys His Glu Ile Asp Ile Arg Leu Ile Lys Phe Gln	
50 55 60 65	
gct gtt gaa aat ggc ttg cct gaa ggt tgt gag cgt att gat ctt atc	356
Ala Val Glu Asn Gly Leu Pro Glu Gly Cys Glu Arg Ile Asp Leu Ile	
70 75 80	
cct tct gat gac aag ctt tcc aat ttt ttg aaa gct gca gct atg atg	404
Pro Ser Asp Asp Lys Leu Ser Asn Phe Leu Lys Ala Ala Ala Met Met	
85 90 95	
caa gaa cca ctt gag cag ctt att gaa gaa tgt cat ccc aat tgt ctt	452
Gln Glu Pro Leu Glu Gln Leu Ile Glu Glu Cys His Pro Asn Cys Leu	
100 105 110	
gtt tct gat atg ttc ctt cct tgg act act gat act gca gcc aag ttt	500
Val Ser Asp Met Phe Leu Pro Trp Thr Thr Asp Thr Ala Ala Lys Phe	
115 120 125	
aac att cca aga ata gtt ttc cat ggt acg agt ttc ttt gca ctt tgt	548
Asn Ile Pro Arg Ile Val Phe His Gly Thr Ser Phe Phe Ala Leu Cys	
130 135 140 145	
gta gag aat agt aac agg act aat aag cca ttc aag aac gtc tct tct	596
Val Glu Asn Ser Asn Arg Thr Asn Lys Pro Phe Lys Asn Val Ser Ser	
150 155 160	
gat tct gaa act ttt gtt gta cca aat ttg cct cac gaa atc agg cta	644
Asp Ser Glu Thr Phe Val Val Pro Asn Leu Pro His Glu Ile Arg Leu	
165 170 175	

act aga aca caa ttg tct ccg ttt gag caa tca ttg gaa gag aca cca	692
Thr Arg Thr Gln Leu Ser Pro Phe Glu Gln Ser Leu Glu Glu Thr Pro	
180 185 190	
atg tcc cga atg ata aaa gca gtt agg gaa tcg gac gcg aag agt tat	740
Met Ser Arg Met Ile Lys Ala Val Arg Glu Ser Asp Ala Lys Ser Tyr	
195 200 205	
gga gtt atc ttc aac agc ttc tat gag ctt gaa tca gat tat gtt gaa	788
Gly Val Ile Phe Asn Ser Phe Tyr Glu Leu Glu Ser Asp Tyr Val Glu	
210 215 220 225	
cat tat acc aag gtt ctt ggt aga aag tct tgg gct att ggc ccg ctt	836
His Tyr Thr Lys Val Leu Gly Arg Lys Ser Trp Ala Ile Gly Pro Leu	
230 235 240	
tct ttg tgc aat agg gac att gaa gat aaa gct gaa aga ggg aag att	884
Ser Leu Cys Asn Arg Asp Ile Glu Asp Lys Ala Glu Arg Gly Lys Ile	
245 250 255	
tcc tct att gat aaa cat gag tgt ttg aat tgg ctt gat tca aag aaa	932
Ser Ser Ile Asp Lys His Glu Cys Leu Asn Trp Leu Asp Ser Lys Lys	
260 265 270	
cca agt tcc att gtt tat gtt tgc ttc ggg agc gta gca gat ttc act	980
Pro Ser Ser Ile Val Tyr Val Cys Phe Gly Ser Val Ala Asp Phe Thr	
275 280 285	
gca gca caa atg cgt gaa ctt gca ttg gga att gaa gca tct gga caa	1028
Ala Ala Gln Met Arg Glu Leu Ala Leu Gly Ile Glu Ala Ser Gly Gln	
290 295 300 305	
gaa ttc att tgg gct gtt aga aga ggc aaa gag gaa caa gac aat gaa	1076
Glu Phe Ile Trp Ala Val Arg Arg Gly Lys Glu Glu Gln Asp Asn Glu	
310 315 320	
gag tgg ttg cct gaa gga ttc gag gaa aga acg aaa gaa aaa ggt cta	1124
Glu Trp Leu Pro Glu Gly Phe Glu Glu Arg Thr Lys Glu Lys Gly Leu	
325 330 335	
att att aga gga tgg gcg ccc caa gtg cta att ctt gat cac caa gct	1172
Ile Ile Arg Gly Trp Ala Pro Gln Val Leu Ile Leu Asp His Gln Ala	
340 345 350	
gtg gga gct ttt gtc act cat tgt ggt aat tca acg ctt gaa gga	1220
Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu Glu Gly	
355 360 365	

gta tca gca ggg gtg cct atg gtg acc tgg cct gtg ttt gca gag caa	1268		
Val Ser Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala Glu Gln			
370	375	380	385
ttt ttc aat gaa aag ttg gtg act gag gtt ttg aga act ggg gct ggt	1316		
Phe Phe Asn Glu Lys Leu Val Thr Glu Val Leu Arg Thr Gly Ala Gly			
390	395	400	
gtt ggt tca atg caa tgg aaa aga tca gct agc gag gga gta aaa agg	1364		
Val Gly Ser Met Gln Trp Lys Arg Ser Ala Ser Glu Gly Val Lys Arg			
405	410	415	
gaa gca ata gct aag gca ata aag aga gtc atg gtg agt gaa gaa gca	1412		
Glu Ala Ile Ala Lys Ala Ile Lys Arg Val Met Val Ser Glu Glu Ala			
420	425	430	
gag gga ttc aga aac cga gct aaa gcc tac aaa gag atg gca aaa caa	1460		
Glu Gly Phe Arg Asn Arg Ala Lys Ala Tyr Lys Glu Met Ala Lys Gln			
435	440	445	
gct att gaa gaa gga gga tct tct tac tct gga ttg act act ttg cta	1508		
Ala Ile Glu Glu Gly Ser Ser Tyr Ser Gly Leu Thr Thr Leu Leu			
450	455	460	465
caa gat ata agt aca tat agt tcc aaa agt cat taactgcaca actaaaaaaaa	1561		
Gln Asp Ile Ser Thr Tyr Ser Ser Lys Ser His			
470	475		
tgttgttttgg ttctatacaa tttttatgct tttttatgcg tgtactaatt taaacatgga	1621		
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<223> Amino acid sequence of a protein having glycosyl transferase to aurone

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 Lys Ala Thr Ile Ile Thr Thr Pro Leu Asn Glu Ser Val Phe Ser Lys
 35 40 45
 Ala Ile Glu Arg Asn His Glu Ile Asp Ile Arg Leu Ile Lys Phe
 50 55 60
 Gln Ala Val Glu Asn Gly Leu Pro Glu Gly Cys Glu Arg Ile Asp Leu
 65 70 75 80
 Ile Pro Ser Asp Asp Lys Leu Ser Asn Phe Leu Lys Ala Ala Met
 85 90 95
 Met Gln Glu Pro Leu Glu Gln Leu Ile Glu Glu Cys His Pro Asn Cys
 100 105 110
 Leu Val Ser Asp Met Phe Leu Pro Trp Thr Thr Asp Thr Ala Ala Lys
 115 120 125
 Phe Asn Ile Pro Arg Ile Val Phe His Gly Thr Ser Phe Phe Ala Leu
 130 135 140
 Cys Val Glu Asn Ser Asn Arg Thr Asn Lys Pro Phe Lys Asn Val Ser
 145 150 155 160
 Ser Asp Ser Glu Thr Phe Val Val Pro Asn Leu Pro His Glu Ile Arg
 165 170 175
 Leu Thr Arg Thr Gln Leu Ser Pro Phe Glu Gln Ser Leu Glu Glu Thr
 180 185 190
 Pro Met Ser Arg Met Ile Lys Ala Val Arg Glu Ser Asp Ala Lys Ser
 195 200 205
 Tyr Gly Val Ile Phe Asn Ser Phe Tyr Glu Leu Glu Ser Asp Tyr Val
 210 215 220
 Glu His Tyr Thr Lys Val Leu Gly Arg Lys Ser Trp Ala Ile Gly Pro
 225 230 235 240
 Leu Ser Leu Cys Asn Arg Asp Ile Glu Asp Lys Ala Glu Arg Gly Lys
 245 250 255
 Ile Ser Ser Ile Asp Lys His Glu Cys Leu Asn Trp Leu Asp Ser Lys
 260 265 270
 Lys Pro Ser Ser Ile Val Tyr Val Cys Phe Gly Ser Val Ala Asp Phe
 275 280 285
 Thr Ala Ala Gln Met Arg Glu Leu Ala Leu Gly Ile Glu Ala Ser Gly
 290 295 300
 Gln Glu Phe Ile Trp Ala Val Arg Arg Gly Lys Glu Glu Gln Asp Asn
 305 310 315 320

Glu Glu Trp Leu Pro Glu Gly Phe Glu Glu Arg Thr Lys Glu Lys Gly
325 330 335
Leu Ile Ile Arg Gly Trp Ala Pro Gln Val Leu Ile Leu Asp His Gln
340 345 350
Ala Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu Glu
355 360 365
Gly Val Ser Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala Glu
370 375 380
Gln Phe Phe Asn Glu Lys Leu Val Thr Glu Val Leu Arg Thr Gly Ala
385 390 395 400
Gly Val Gly Ser Met Gln Trp Lys Arg Ser Ala Ser Glu Gly Val Lys
405 410 415
Arg Glu Ala Ile Ala Lys Ala Ile Lys Arg Val Met Val Ser Glu Glu
420 425 430
Ala Glu Gly Phe Arg Asn Arg Ala Lys Ala Tyr Lys Glu Met Ala Lys
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22

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23